



PT for identifying modulators useful for treating a disease or condition  
 PT mediated by human transporter protein -  
 PS Claim 1; Fig 2; 200pp; English.

CC The present sequence is a human transporter protein, which is related to  
 CC the sodium/calcium exchanger subfamily. Experimental data indicates  
 CC expression of the transporter gene in humans in brain, heart, kidney,  
 CC lung, spleen, testis, leukocyte and foetal brain. The gene of the  
 CC transporter was mapped to chromosome 14 by ePCR.

XX Sequence 921 AA;

Query Match 100.0%; Score 4797; DB 23; Length 921;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMRLDPLTSAFLHFGVLFVFLNGLRABAGSGDVPSTGQNNESGSSDCKEGVIL 60  
 DB 1 MAMRLDPLTSAFLHFGVLFVFLNGLRABAGSGDVPSTGQNNESGSSDCKEGVIL 60  
 QY 61 PIWPEPNSLGDKTARVIVFVALIYMFVLSIADRFMASTIEVTSQEREVTIKKPNGE 120  
 DB 61 PIWPEPNSLGDKTARVIVFVALIYMFVLSIADRFMASTIEVTSQEREVTIKKPNGE 120  
 QY 121 TSTTIRWNETVSNLTLMALGSSAPETILSLIEVCGHGFAGDLGPSTIVGSAFNMFI 180  
 DB 121 TSTTIRWNETVSNLTLMALGSSAPETILSLIEVCGHGFAGDLGPSTIVGSAFNMFI 180  
 QY 181 IIGICVYVPIPGETRIKHLNVEFTTAAMSTFAYITWLMILAVSPGVQVWEGILLTFE 240  
 DB 181 IIGICVYVPIPGETRIKHLNVEFTTAAMSTFAYITWLMILAVSPGVQVWEGILLTFE 240  
 QY 241 FPVCVLLAMVADKRLLEFKYMKKYPRTDKHGIIEETGDPKGIEMGKMNNSFLDGN 300  
 DB 241 FPVCVLLAMVADKRLLEFKYMKKYPRTDKHGIIEETGDPKGIEMGKMNNSFLDGN 300  
 QY 301 LVPLEGKEVDSESRREMTIRILDKOKHPEKDLQLEVMANLYALSHOQSRAFYRIQATR 360  
 DB 301 LVPLEGKEVDSESRREMTIRILDKOKHPEKDLQLEVMANLYALSHOQSRAFYRIQATR 360  
 QY 361 MMTAGNLTAKHAADQAKKASMSSEVHTDEPEDTSKYFPDPCSTQCLNCGAVLLVVR 420  
 DB 361 MMTAGNLTAKHAADQAKKASMSSEVHTDEPEDTSKYFPDPCSTQCLNCGAVLLVVR 420  
 QY 421 KGGDMSTMYVDYKTEGDSANAGADYEFTTEGTVLAKPEETOKESVGIIDDDIFEEDHFE 480  
 DB 421 KGGDMSTMYVDYKTEGDSANAGADYEFTTEGTVLAKPEETOKESVGIIDDDIFEEDHFE 480  
 QY 481 FVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVITLDDDHAGIIFTECDTIH 540  
 DB 481 FVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVITLDDDHAGIIFTECDTIH 540  
 QY 541 VSESIGWAEVAVLTSGARGTVIYPERIVESTAKGGEDFDYTGELFEKNDYVKTIRV 600  
 DB 541 VSESIGWAEVAVLTSGARGTVIYPERIVESTAKGGEDFDYTGELFEKNDYVKTIRV 600  
 QY 601 KIYDEEYEROEENFFIALGEPKMERGISDVTDRKLTMEEBEAKRIEMGKPVVGEHPKL 660  
 DB 601 KIYDEEYEROEENFFIALGEPKMERGISDVTDRKLTMEEBEAKRIEMGKPVVGEHPKL 660  
 QY 661 EVIIEESYEFTTVDKLTKTNLALVYGTSHWRDQFMEAITVSAAGDEDESEGERLPS 720  
 DB 661 EVIIEESYEFTTVDKLTKTNLALVYGTSHWRDQFMEAITVSAAGDEDESEGERLPS 720  
 QY 721 CFVDVYMFELTYFKKVLFRACVPTEYCHGWACFAVSIILIGMLTAIIGDLASHFECTIGLK 780  
 DB 721 CFVDVYMFELTYFKKVLFRACVPTEYCHGWACFAVSIILIGMLTAIIGDLASHFECTIGLK 780  
 QY 781 DSVTAAYVFVAGTGVPTDFASKAALADVDVADASIGNVTGSNANVFLGILASVAAIY 840  
 DB 781 DSVTAAYVFVAGTGVPTDFASKAALADVDVADASIGNVTGSNANVFLGILASVAAIY 840

QY 841 WALOGQEFHVSAGTLAFSVLTFTTFAFVCSIVLLYRRRPHLGELGPRGCKLATWMLFV 900  
 DB 841 WALOGQEFHVSAGTLAFSVLTFTTFAFVCSIVLLYRRRPHLGELGPRGCKLATWMLFV 900  
 QY 901 SLMLLYILFATLEAVCYIKGF 921  
 DB 901 SLMLLYILFATLEAVCYIKGF 921

# RESULT 2

AA047745

AA047745 standard; Protein: 927 AA.

AC AA047745;

XX 25-FEB-2002 (first entry)

XX Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3.

XX Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;

XX cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;

XX myocarditis; pulmonary hypertension; cardiotoxicity; cardiac; Vaccine;

XX coronary heart disease; renal failure; ischaemic disorder;

XX Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder.

XX Homo sapiens.

XX W0200183744-A2.

XX 08-NOV-2001.

XX 30-APR-2001; 2001MO-EP04886.

XX 02-MAY-2000; 2000EP-0109080.

XX (MERE ) MERCK PATENT GMBH.

XX Wilm C;

XX WPI: 2002-0041493/05.

XX N-PSDB: ABA04756.

XX New polypeptide, useful as vaccines for inducing immune response

XX against diseases such as myocardial infarction, arrhythmia, ischemic

XX disorders, renal disorders in mammal -

XX Claim 1; Page 38-41; 41pp; English.

XX The present sequence is the protein sequence for human Natrium(+)-Calcium

XX (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome

XX 14. HNCX3 and its coding sequence are useful for treating acute and

XX chronic cardiac failure of different aetiologies, myocardial infarction,

XX cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,

XX cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,

XX acute and chronic renal failure, ischaemic disorders of skeletal muscle

XX and ischaemic brain disorders of different aetiologies.

QY Sequence 927 AA;

Query Match 99.7%; Score 4784; DB 23; Length 927;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 921; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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Db 121 TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLPSTIVGSAFNMFI 180
Qy 181 IIGICVYVIPDGETRKIKHLRVFEFTAAMSIFAYIMLWMLAVSPGVQVWEGILLTFE 240
Db 181 IIGICVYVIPDGETRKIKHLRVFEFTAAMSIFAYIMLWMLAVSPGVQVWEGILLTFE 240
Qy 241 FPCVLLAMVADKRLLFYKYMHKKRYRTDKHRIIIEEGDHPKGIEMDKMNSHFLDGN 300
Db 241 FPCVLLAMVADKRLLFYKYMHKKRYRTDKHRIIIEEGDHPKGIEMDKMNSHFLDGN 300
Qy 301 LVPLEGEKVEDESRRMIRILDKOKHPEKIDQLVEMANYALSHOOKSRAFYRIQATR 360
Db 301 LVPLEGEKVEDESRRMIRILDKOKHPEKIDQLVEMANYALSHOOKSRAFYRIQATR 360
Qy 361 MMTGAGNLLKHAADQAKKASSMSSEVHTDEPDFTSKVFEDPCSYOCLENCAGAVLLTVVR 420
Db 361 MMTGAGNLLKHAADQAKKASSMSSEVHTDEPDFTSKVFEDPCSYOCLENCAGAVLLTVVR 420
Qy 421 KGDMSKTMVYDYKTEDGSANAGADYEFTGTVLKPGETOKEFVSIGIIDDIFEEDEF 480
Db 421 KGDMSKTMVYDYKTEDGSANAGADYEFTGTVLKPGETOKEFVSIGIIDDIFEEDEF 480
Qy 481 FVRLSNVRIEEBQEPREGMPALFNSLPPLRAVLASPCVATVITLDDHAGIFTFECDTIH 540
Db 481 FVRLSNVRIEEBQEPREGMPALFNSLPPLRAVLASPCVATVITLDDHAGIFTFECDTIH 540
Qy 541 VSESIGVMEVKVLRITSGARGTVIPEPRIVEGTAKGGGEDEFTYGELEFKNDETYKTIHV 600
Db 541 VSESIGVMEVKVLRITSGARGTVIPEPRIVEGTAKGGGEDEFTYGELEFKNDETYKTIHV 600
Qy 601 KIVDEEERENFIALGEPKMERGIS-----DVTDRKLTMEEEBAKRIEMGKPYL 654
Db 601 KIVDEEERENFIALGEPKMERGISGVAFKDYVDTRKLTMEEEBAKRIEMGKPYL 660
Qy 655 GEHPRLEVIIEESYEFTKTVDKLIKKTMLALVVGTHSMRDQMEAITVSAAGDEDEDESG 714
Db 655 GEHPRLEVIIEESYEFTKTVDKLIKKTMLALVVGTHSMRDQMEAITVSAAGDEDEDESG 720
Qy 715 EERLPSCEVDYVNHFTLVYWKVLFACVPRPEYCHGWACRAVSLIITGMLTATIGDLASHHG 774
Db 715 EERLPSCEVDYVNHFTLVYWKVLFACVPRPEYCHGWACRAVSLIITGMLTATIGDLASHHG 780
Qy 775 CTIGLSDVTAVFAFGTSVDPTEFASKAALQDYADASIGNVGTGNNANVYFLGIGLAM 834
Db 775 CTIGLSDVTAVFAFGTSVDPTEFASKAALQDYADASIGNVGTGNNANVYFLGIGLAM 840
Qy 835 SVAALYMALQGEFHVSAAGTLAFSVTLFTFAFVCISVLLYRRRPHLGELGGPRGCKLA 894
Db 835 SVAALYMALQGEFHVSAAGTLAFSVTLFTFAFVCISVLLYRRRPHLGELGGPRGCKLA 900
Qy 895 TTWLFVSLMLLYILFATLEAYCYIKGF 921
Db 895 TTWLFVSLMLLYILFATLEAYCYIKGF 927

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RESULT 3  
 ABB83247  
 ID ABB83247 standard; Protein: 927 AA.

XX ABB83247;  
 XX 21-AUG-2002 (first entry)  
 XX Human transporter protein-related protein, used in a homology alignment.  
 XX Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;  
 KW spleen; testis; leukocyte; foetal brain; chromosome 14.  
 XX Unidentified.  
 OS  
 XX WO200233086-A2.  
 PN  
 XX 25-APR-2002.  
 PD

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XX 17-OCT-2001; 2001WO-US32152.
PF
XX 17-OCT-2000; 2000US-240836P.
PR
XX 13-MAR-2001; 2001US-0804474.
XX
XX (PEKE ) PE CORP NY.
PA
PI Metulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;
PI Beasley EM;
PI WPI; 2002-479677/51.
PT Human transporter peptide related to sodium/calcium exchanger subfamily
PT for identifying modulators useful for treating a disease or condition
PT mediated by human transporter protein
PS
XX Disclosure: Fig 2; 200pp; English.
CC The present invention relates to a human transporter protein, which is
CC related to the sodium/calcium exchanger subfamily (ABB83246).
CC Experimental data indicates expression of the transporter gene in humans
CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR.
CC The present protein was used in a sequence alignment with the transporter
CC protein to illustrate the invention.
SQ
XX Sequence 927 AA:
Query Match 97.7%; Score 4686; DB 23; Length 927;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 897; Conservative 14; Mismatches 10; Indels 6; Gaps 1;
Qy 1 MAMRLQPLTSALFHLGTVFLVFLNGLRAEAGSGDYVSTGONNESCSSDCKEGVIL 60
Db 1 MAMRLQPLTSALFHLGTVFLVFLNGLRAEAGDLRDVPSAGONNESCSSDCKEGVIL 60
Qy 61 PIWYEPNPSLGKIRAVIYFVALIYMFGLVSTIADRFMASTIEVTSOREVYTIKKPNE 120
Db 61 PIWYEPNPSLGKIRAVIYFVALIYMFGLVSTIADRFMASTIEVTSOREVYTIKKPNE 120
Qy 121 TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLPSTIVGSAFNMFI 180
Db 121 TSTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLPSTIVGSAFNMFI 180
Qy 181 IIGICVYVIPDGETRKIKHLRVFEFTAAMSIFAYIMLWMLAVSPGVQVWEGILLTFE 240
Db 181 IIGICVYVIPDGETRKIKHLRVFEFTAAMSIFAYIMLWMLAVSPGVQVWEGILLTFE 240
Qy 241 FPCVLLAMVADKRLLFYKYMHKKRYRTDKHRIIIEEGDHPKGIEMDKMNSHFLDGN 300
Db 241 FPCVLLAMVADKRLLFYKYMHKKRYRTDKHRIIIEEGDHPKGIEMDKMNSHFLDGN 300
Qy 301 LVPLEGEKVEDESRRMIRILDKOKHPEKIDQLVEMANYALSHOOKSRAFYRIQATR 360
Db 301 LVPLEGEKVEDESRRMIRILDKOKHPEKIDQLVEMANYALSHOOKSRAFYRIQATR 360
Qy 361 MMTGAGNLLKHAADQAKKASSMSSEVHTDEPDFTSKVFEDPCSYOCLENCAGAVLLTVVR 420
Db 361 MMTGAGNLLKHAADQAKKASSMSSEVHTDEPDFTSKVFEDPCSYOCLENCAGAVLLTVVR 420
Qy 421 KGDMSKTMVYDYKTEDGSANAGADYEFTGTVLKPGETOKEFVSIGIIDDIFEEDEF 480
Db 421 KGDMSKTMVYDYKTEDGSANAGADYEFTGTVLKPGETOKEFVSIGIIDDIFEEDEF 480
Qy 481 FVRLSNVRIEEBQEPREGMPALFNSLPPLRAVLASPCVATVITLDDHAGIFTFECDTIH 540
Db 481 FVRLSNVRIEEBQEPREGMPALFNSLPPLRAVLASPCVATVITLDDHAGIFTFECDTIH 540
Qy 541 VSESIGVMEVKVLRITSGARGTVIPEPRIVEGTAKGGGEDEFTYGELEFKNDETYKTIHV 600
Db 541 VSESIGVMEVKVLRITSGARGTVIPEPRIVEGTAKGGGEDEFTYGELEFKNDETYKTIHV 600

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QY 844 OQOEHVSAAGTAAVSTLTFTFAVCISVLYLRRRPHLGELGSGPRGCKLATWLVSLW 903  
DB 893 NQOQFVSVSGTLAFTVSTLTFTFAVGVLLVRRRPEIGELGSGPRATKLITSCLEVLW 952  
QY 904 LYLIFATLEANCYKGF 921  
DB 953 LLYFFSSLEAVCHIKGF 970

RESULT 5  
AAB41497  
ID AAB41497 standard; Protein; 952 AA.  
AC AAB41497;  
XX  
XX 08-FEB-2001 (first entry)  
DE Human ORFX ORF1261 polypeptide sequence SEQ ID NO:2522.  
XX  
XX Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;  
XX vulnary; antipruritic; antiparkinsonian; nootropic; neuroprotective;  
XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
XX hypotensive; dermatological; immunosuppressive; antiinflammatory;  
XX antiviral; antibacterial; antifungal; antineumatic; antihypertoid;  
XX antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;  
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
XX cholesterol ester storage; systemic lupus erythematosus; infection;  
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
XX bone damage; cartilage damage; antinflammatory disease; coagulation;  
XX thrombosis; contraceptive.

OS Homo sapiens.  
XX  
XX WO20058473-A2.  
XX  
XX 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000MO-US08621.  
XX  
XX 31-MAR-1999; 99US-0127607.  
XX PR 02-APR-1999; 99US-0127636.  
XX PR 05-APR-1999; 99US-0127728.  
XX PR 30-MAR-2000; 2000US-0540763.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shinkets RA, Leach M;  
XX  
XX WPI: 2000-602362/57.  
XX N-PSDB: AACT5706.  
XX  
XX Novel nucleic acids and peptides derived from open reading frame X,  
XX useful for treating e.g. cancers, proliferative disorders,  
XX neurodegenerative disorders and cardiovascular disease -  
XX  
XX Claim 11: Page 1809-1812; 5507pp; English.

AACT4446 to AACT7606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;  
CC antipruritic; antiparkinsonian; nootropic; neuroprotective;  
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antiinflammatory; antibacterial; antifungal; antineumatic; antihypertoid;  
CC antithyroid; and antianemic. The sequences can be used for determining  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an ORFX-associated disorder. The  
CC nucleic acids can be used to express ORFX proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,

CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX  
XX Sequence 952 AA:  
SQ  
Query Match 70.3%; Score 3373.5; DB 21; Length 952;  
Best local Similarity 71.0%; Pred. No. 0;  
Matches 638; Conservative 124; Mismatches 104; Indels 33; Gaps 9;

QY 40 STGONNCSGSSDCKEGVILPIWYBPNSLQKIAVYVYVALYIMFGVSIADREM 99  
DB 70 STG-----GCQSYRCQPGVLLPVWEPDDPSLQKAAVAVYFVAVYMFVGSIIADRFM 125  
QY 100 ASIEVITTSOREVYTIKKPNETSTTIRVNNVSNLTLMALGSSAPEILLSEVCGHG 159  
DB 126 AAIEVITTSOREVYTIKKPNETSTTIRVNNVSNLTLMALGSSAPEILLSEVCGHG 185  
QY 160 FIAGDGPSTVSAFNFNFIIGICVYVYVDETRIKHLRFYFTAAVSIYVLYM 219  
DB 186 FQAGELGPGTVSAFNFNFIIGICVYVYVDETRIKHLRFYFTAAVSIYVLYM 245  
QY 220 ILAVSPGVVQWEGLLTFEPFVYVLANVADKRLFYKMKYRTDKHRIIETEG 279  
DB 246 ILAVSPGVVQWEGLLTFEPFVYVLANVADKRLFYKMKYRTDKHRIIETEG 305  
QY 280 DHPKGIEMCKMNNHFLQNL-----VPLEGKGVDESREMRILDKQKHPKEDLQ 334  
DB 306 DHPKGIEMCKMNNHFLQNL-----VPLEGKGVDESREMRILDKQKHPKEDLQ 364  
QY 335 LVMANVYALSHOQSRAPFRIQATRMGTGAGNLLKHAQAQKASMSSEVTEDEDF 394  
DB 365 LVGIANVYALSHOQSRAPFRIQATRMGTGAGNLLKHAQAQKASMSSEVTEDEDF 423  
QY 395 ISKVFFDPCSYQCLNCGAVLLTVVRKGDMSKTMVYDYKTEGSGANAGDYFTGTV 454  
DB 424 ASRIFFEPSPSLYHCLNCGSVLLSVTCQCGSGNSTFYVYRTEDGSAKAGSDEYSEGTIV 483  
QY 455 LKPGETOKERSVGIIIDDDIFEEDHEFFVRLSNVRIEEQ-----PEGMPAIFNSLPLR 510  
DB 484 FKPGETOKERLIGIIDDIDFEEDHEFFVRLSNVRIEEQ-----PEGMPAIFNSLPLR 534  
QY 511 AVLASPCVATVTLDDDHAGIIFTECDTIVHSEISIGMEVYVRLTSGARCTVIYVPTVE 570  
DB 535 GRVAPLPLATVTLDDDHAGIIFTECDTIVHSEISIGMEVYVRLTSGARCTVIYVPTVE 594  
QY 571 GTAKGGGEDEFTYGELEFNDETVKTIKIVDEEYERQENFTALGEPKMMERGISO 630  
DB 595 GTARGGVHVEDACGELEFEDDETMTLQVYKIVDEEYERQENFTALGEPKMMERGISO 654  
QY 631 VT-----DRKLMEERBEAKRIAMKGRPVLEHPRKLEVTIEEYERKTYTDKIKTNLA 684  
DB 655 LLLNQGDDGDKRLAEEERARIAEMKRPVLEHPRKLEVTIEEYERKTYTDKIKTNLA 714  
QY 685 LVVGTSMRDQFMEATITVSAAGDEDEDESG--SEERLSPCDFYVNHFTVPMKVLACVPP 742  
DB 715 LVVGTSMRDQFMEATITVSAAGDEDEDESG--SEERLSPCDFYVNHFTVPMKVLACVPP 773  
QY 743 TEYCHGWACFVAVSILITGMLTALIGDLASHFGCTIGLKSVDVAVVAFGTSVDFPASK 802  
DB 774 TEYCHGWACFVAVSILITGMLTALIGDLASHFGCTIGLKSVDVAVVAFGTSVDFPASK 833  
QY 803 AAALQVYVADASIGNTGSAVAVVFLGIGLAVVAITVYALQOEFHVSACTAFSVTLF 862  
DB 834 VAALQVYVADASIGNTGSAVAVVFLGIGLAVVAITVYALQOEFHVSACTAFSVTLF 893  
QY 863 TIFAFCISVLLRRRPHLGELGSGPRGCKLATWLVSLWLVSLWLVSLWLVSLWLVSLW 921





Db 426 LENCQVALTLTIIRGGDLTNVDFVDEREDGTANAGSDYEFTEGTVFKPGDTOKEIRVG 485  
Qy 468 IIDDIFEEDEHFVRLSNVRIEEQPEGMPPAIFNSLPBRAVLASPCVATVITLDD 527  
Db 486 IIDDIFEEDEHFVRLSNVRIEEQPEGMPPAIFNSLPBRAVLASPCVATVITLDD 542  
Qy 528 HAGITFECDTIHVESIGMEVKVLRGARGTVIVPFRVEGTAKGGEDFEDTYGEL 587  
Db 543 HAGITFECDTIHVESIGMEVKVLRGARGTVIVPFRVEGTAKGGEDFEDTYGEL 602  
Qy 588 EFKNDE 593  
Db 603 EFKNDE 608

RESULT 9  
AAM13701  
ID AAM13701 standard; Protein: 609 AA.  
AC AAM13701;  
XX 12-OCT-2001 (first entry)  
XX Peptide #135 encoded by probe for measuring cervical gene expression.  
DE Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer.  
XX Homo sapiens.  
OS  
XX W0200157278-A2.  
FN  
XX 09-AUG-2001.  
PD  
XX 30-JAN-2001; 2001MO-US00670.  
PF  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488901/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human cervical epithelial cells -  
XX  
XX Claim 27; SEQ ID No 18527; 487bp; English.  
XX  
XX The present invention relates to human single exon nucleic acid probes  
CC (SNP: see AAI10068-AA128459). The present sequence is a peptide encoded  
CC by one such probe. The SNPs are derived from human Hela cells. The SNPs  
CC can be used to produce a single exon microarray, which can be used for  
CC measuring human gene expression in a sample derived from human cervical  
CC epithelial cells. By measuring gene expression, the probes are therefore  
CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 609 AA;  
SQ

Query Match 44.7%; Score 2143.5; DB 22; Length 609;  
Best Local Similarity 69.3%; Pred. NO. 6.9e-200;  
Matches 420; Conservative 76; Mismatches 89; Indels 21; Gaps 8;

Qy 1 MAMRLQPLTSAFLEHGLVTEVLF--LNGLRAGAGSGDVPSTGONNESCSSGSDPKCGV 58  
Db 11 MRRSLSTFTSMGFFLLTVTSILTSFVSHVDYIAETEMEBEGNETG---CIGSYCCKGGV 66  
Qy 59 ILPIWYENPNSLGDKIARVIVYFVALIYMETGVSIADREMASEIVTSGREYTIKKPN 118  
Db 67 ILPIWEPQDPSFGCIKARATYFVAMVYMFGLVSIADREMASEIVTSGREYTIKKPN 126  
Qy 119 GETSTTIRVNNENYTNLTMAIGSSAPEILLSIENCGHGFINGDGPSTIVSAFNM 178  
Db 127 GETTKTVIRNNETVSNLTMAIGSSAPEILLSIENCGHGFINGDGPSTIVSAFNM 186  
Qy 179 FIIGICVYVIPDGETRKIKLRVEFFITAMSIPIAYIWLXMIILAVFSPGVQVWEGLLTL 238  
Db 187 FIITIALCYVVPDGETRKIKLRVEFFITAMSIPIAYIWLXMIILAVFSPGVQVWEGLLTL 246  
Qy 239 FFFPVCVLLANVADKRLLFYKMKKRTDKHGIITTEGDRKG--IMDGKMANSH 295  
Db 247 FFFPVCVLLANVADKRLLFYKMKKRTDKHGIITTEGDRKG--IMDGKMANSH 306  
Qy 296 --FLDGNLVPLEGEVD---ESRREMIRILKDKOKHPKEDLDQVEMANYALSHQ 348  
Db 307 VENFLDGNLV-LEVDERDQDEDEARREMARILKEKQHPKELIQLTFLANYOVLSCQ 365  
Qy 349 KSRAFYRIQATRMGTGACNIIKKHAEDQAKKASSMEVHTDEPE-DFISKVFPDPCSYOC 407  
Db 366 KSRAFYRIQATRMGTGACNIIKKHAEDQAKKASSMEVHTDEPE-DFISKVFPDPCSYOC 425  
Qy 408 LENCQVALTLTIIRGGDLTNVDFVDEREDGTANAGSDYEFTEGTVFKPGDTOKEIRVG 467  
Db 426 LENCQVALTLTIIRGGDLTNVDFVDEREDGTANAGSDYEFTEGTVFKPGDTOKEIRVG 485  
Qy 468 IIDDIFEEDEHFVRLSNVRIEEQPEGMPPAIFNSLPBRAVLASPCVATVITLDD 527  
Db 486 IIDDIFEEDEHFVRLSNVRIEEQPEGMPPAIFNSLPBRAVLASPCVATVITLDD 542  
Qy 528 HAGITFECDTIHVESIGMEVKVLRGARGTVIVPFRVEGTAKGGEDFEDTYGEL 587  
Db 543 HAGITFECDTIHVESIGMEVKVLRGARGTVIVPFRVEGTAKGGEDFEDTYGEL 602  
Qy 588 EFKNDE 593  
Db 603 EFKNDE 608

RESULT 10  
AAM26102  
ID AAM26102 standard; Protein: 609 AA.  
AC AAM26102;  
XX  
XX 17-OCT-2001 (first entry)  
XX  
XX Peptide #139 encoded by probe for measuring placental gene expression.  
DE Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
XX  
XX Homo sapiens.  
OS  
XX W0200157272-A2.  
FN  
XX 09-AUG-2001.  
PD  
XX 30-JAN-2001; 2001MO-US00663.  
PF  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.



PR 04-OCT-2000; 2000GB-0024263.

XX (MOE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX

PT Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human placenta -

CC

PS Claim 27: SEQ ID NO 26371; 654bp; English.

XX

CC The present invention relates to single exon nucleic acid probes (SENPs;

CC see AAI3315-AA157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders.

XX

XX Sequence 609 AA;

Query Match 44.7%; Score 2143.5; DB 22; Length 609;

Best Local Similarity 69.3%; Pred. No. 6.9e-200;

Matches 420; Conservative 76; Mismatches 89; Indels 21; Gaps 8;

QY 1 MAMRLRPLTSAFLHGLVTEVL--LNGLRADAGSGSDVPSTGQNNSSCGSSDCKEGV 58

Db 11 MRLRLSPTFSMGFHLVTVSLFSDVHDVIAETEMEGBNETGE---CTGTYCKKGV 66

QY 59 ILPLTPENPSLGDKIARVIVYFVALITMELGVSIIADRFMASIEVITSQEREYTIKKPN 118

Db 67 ILPLTPEPDPSFGDKIARVIVYFVALITMELGVSIIADRFMASIEVITSQEREYTIKKPN 126

QY 119 GETSTTTRRVNNEVNSNTLMAAGSABEILSLIEVCGHGHTAGDLPSTIVGSAAFNM 178

Db 127 GETTKTYIRINNEVNSNTLMAAGSABEILSLIEVCGHGHTAGDLPSTIVGSAAFNM 186

QY 179 FIILGICVYVIPDGETRRIKHLRVETFAAMSIFAYIMLYMLIAVSPGVQVMEGLTLT 238

Db 187 FIILACVYVVPDGETRRIKHLRVETFAAMSIFAYIMLYMLIAVSPGVQVMEGLTLT 246

QY 239 FFFPVCVLLANVADKRLLFYKIMKKKYTDKRGIIIEGDPKGV--IEMDGKIMNSH 295

Db 247 FFFPVCVFAVAVDRLLFFYKYVYKRYRAGKORGMIIIEGDRPSSKTEIEMDGKIVNSH 306

QY 296 ---FLDGLVLPLEGKVD---ESRREMIRIKDLKOKHREKDDQVEMANYVALSHNQ 348

Db 307 VENFLDGLV--LEVDERODDEAREMARIRIKELKOKHREKDDQVEMANYVALSHNQ 365

QY 349 KSRAFYRIQATRMGTGAGNILLKHAADQAKKASSSEVHTDEPE-DFISKVFFDCSYOC 407

Db 366 KSRAFYRIQATRMGTGAGNILLKHAADQAKKASSSEVHTDEPE-DFISKVFFDCSYOC 425

QY 408 LENCAGVLLTVYVRKGGDSKTYVDYKTEEDGSANAGADYEFTGEGTVVLKPGETQKEFSYG 467

Db 426 LENCAGVLLTVYVRKGGDSKTYVDYKTEEDGSANAGADYEFTGEGTVVLKPGETQKEIRVG 485

QY 468 IIDDIDFEDDHFVRILSNVRIIEEQPREGMPRALFNSILPLRAVLASCAVATVITLDD 527

Db 486 IIDDIDFEDDHFVRILSNVRIIEEQPREGMPRALFNSILPLRAVLASCAVATVITLDD 542

QY 528 HAGITFEPCDTHVSESIGVMEVKVLRTSGAGTIVFPFVEGTAKGGEDEFTDYGEL 587

Db 543 HAGITFEPCDTHVSESIGVMEVKVLRTSGAGTIVFPFVEGTAKGGEDEFTDYGEL 602

QY 588 EFKND 593

Db 603 EFKND 608

RESULT 11

ABG35474

ID	ABG35474	standard; Peptide; 609 AA.
AC	ABG35474.	
XX		
DT	19-AUG-2002	(first entry)
DE		Human peptide encoded by genome-derived single exon probe SEQ ID 25139.
XX		
XX		Human; single exon probe; asthma; lung cancer; COPD; ILD;
OS	Homo sapiens.	
XX		
XX	WO200186003-A2.	
PN		
PD	15-NOV-2001.	
XX		
PF	30-JAN-2001; 2001WO-US00665.	
XX		
PR	04-FEB-2000; 2000US-180312P.	
PR	26-MAY-2000; 2000US-207456P.	
PR	30-JUN-2000; 2000US-0608408.	
PR	03-AUG-2000; 2000US-0632366.	
PR	21-SEP-2000; 2000US-234687P.	
PR	27-SEP-2000; 2000US-236359P.	
PR	04-OCT-2000; 2000GB-0024263.	
XX		
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;	
PT	WPI; 2002-114183/15.	
PT		Spatially-addressable set of single exon nucleic acid probes, used to
PS		measure gene expression in human lung samples -
XX		
XX	claim 27; SEQ ID NO 25139; 634bp; English.	
CC	The invention relates to a spatially-addressable set of single exon	
CC	nucleic acid probes for measuring gene expression in a sample derived	
CC	from human lung comprising single exon nucleic acid probes having one of	
CC	12614 nucleic acid sequences mentioned in the specification, or their	
CC	complements or the 12387 open reading frames derived from the 12614	
CC	probes. Also included are a microarray comprising the novel set of	
CC	probes: the novel set of probes which hybridize at high stringency to a	
CC	nucleic acid expressed in the human lung; measuring gene expression in a	
CC	sample derived from human lung, comprising (a) contacting the array with	
CC	a collection of detectably labeled nucleic acids derived from human	
CC	mRNA, and (b) measuring the label detectably bound to each probe of	
CC	the array; identifying exons in a eukaryotic genome, comprising	
CC	(a) algorithmically predicting at least one exon from genomic sequences	
CC	of the eukaryote; and (b) detecting specific hybridisation of detectably	
CC	labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,	
CC	having a fragment identical to the predicted exon, the probe is included	
CC	in the above mentioned microarray; assigning exons to a single gene,	
CC	comprising (a) identifying exons from genomic sequence by the method	
CC	above and (b) measuring the expression of each of the exons in several	
CC	tissues and/or cell types using hybridisation to a single exon	
CC	microarrays having a probe with the exon, where a common pattern of	
CC	expression of the exons in the tissues and/or cell types indicates that	
CC	the exons should be assigned to a single gene; a peptide comprising one	
CC	of 12011 sequences, mentioned in the specification, or encoded by the	
CC	probes/open reading frames (ORF). The probes are used for gene	
CC	expression analysis, and for identifying exons in a gene, particularly	
CC	using human lung derived mRNA and for the study of lung diseases	
CC	such as asthma, lung cancer, chronic obstructive pulmonary disease	
CC		

CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-Pick disease, Hemaneky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemodierosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Kartagener syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 609 AA;

Query Match 44.7%; Score 2143.5; DB 23; Length 609;  
 Best Local Similarity 69.3%; Pred. No. 6.9e-200;

Matches 420; Conservative 76; Mismatches 89; Indels 21; Gaps 8;

QY 1 MAMRLQPLTSAPLHFGVLPFLF--LNGLRAGSGSDVPTGCONNCSGSSDCKEGV 58  
 DB 11 MRRLSLSPTSMGFHLVTVSLFSHVDVIAETEMEGNETGE---CTGSYCKKGV 66  
 QY 59 ILPLTPENPSLCKIARVYFYALIMFLGVSIIADREMASIEVITTSQREVTIKPN 118  
 DB 67 ILPLTPEDPSFGDKIARATYFVAMVYMLGVSIIADREMSIEVITTSQREVTIKPN 126  
 QY 119 GETSTTIRVWNETVSNLTLMALGSSAPETLSIEVCGHGFITGDIAGSPSTVSAFNM 178  
 DB 127 GETTKTVIRINETVSNLTLMALGSSAPETLSIEVCGHGFITGDIAGSPSTVSAFNM 186  
 QY 179 FIIGICVYVDPDETRIKHLRVFETTAWSIFAYIMLYMILAVFSPGVQVEGLTTL 238  
 DB 187 FIILACVYVDPDETRIKHLRVFETTAWSIFAYIMLYMILAVFSPGVQVEGLTTL 246  
 QY 239 FFFVVCVLLAVNADKRLFFYMKKRTDKRGIIETEDDKRG---IEMDKMNSH 295  
 DB 247 FFFVVCVFAVAVNADKRLFFYMKKRTDKRGIIETEDDKRG---IEMDKMNSH 306  
 QY 296 ---FLDGNLPLLEGEKVD---ESRREIRILDKOKHPKEDDOLVEMANYALSHQ 348  
 DB 307 VENLDGALV-LEVDERDQDEEARREMARILKELKOKHPKEDDOLVEMANYALSHQ 365  
 QY 349 KSRAFYRIQATRMATGAGNLIKHAADQAKKASSMEVHDEPE-DFISKVFFDPCSYOC 407  
 DB 366 KSRAFYRIQATRMATGAGNLIKHAADQAKKASSMEVHDEPE-DFISKVFFDPCSYOC 425  
 QY 408 LENGAVLLTVVRKGGMSKTMVDTKTEDGSANAGADYETECTVYLAKPEOTKESYV 467  
 DB 426 LENGAVLLTVVRKGGMSKTMVDTKTEDGSANAGADYETECTVYLAKPEOTKESYV 485  
 QY 468 IIDDIFEEDHEFVRLSNVRIIEEPEEGMPAIFNSLPLRAVLASPCVATYTIIDD 527  
 DB 486 IIDDIFEEDHEFVRLSNVRIIEEPEEGMPAIFNSLPLRAVLASPCVATYTIIDD 542  
 QY 528 HAGIFTECDTIHVESIGVAVKRLTSGARGTVIVPFTVEGTANGGGEDEFTYGE 587  
 DB 543 HAGIFTECDTIHVESIGVAVKRLTSGARGTVIVPFTVEGTANGGGEDEFTYGE 602  
 QY 588 EFKNDE 593  
 DB 603 EFKNDE 608

RESULT 12

ABB61721

XX ID ABB61721 standard; Protein; 950 AA.

XX AC ABB61721;

XX DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 11955.

XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL05824.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -

PS Disclosure; SEQ ID NO 11955; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 950 AA;

Query Match 44.4%; Score 2130.5; DB 22; Length 950;  
 Best Local Similarity 49.2%; Pred. No. 2.8e-198;

Matches 436; Conservative 160; Mismatches 235; Indels 56; Gaps 16;

QY 53 DCKSGVLLPIWYR-NSLGDKIARVYFYALIMFLGVSIIADREMASIEVITTSQRE 111  
 DB 99 ECKSGVLLPIWYR-NSLGDKIARVYFYALIMFLGVSIIADREMASIEVITTSQRE 158  
 QY 112 VTIRKPNGETSTTIRVWNETVSNLTLMALGSSAPETLSIEVCGHGFITAGDLPSTIV 171  
 DB 159 VYVAGPNTKQVMIRVNETVSNLTLMALGSSAPETLSIEVCGHGFITAGDLPSTIV 218  
 QY 172 GSAAFNMFIIIGICVYVDPDETRIKHLRVFETTAWSIFAYIMLYMILAVFSPGVQV 231  
 DB 219 GSAAFNMFIIIGICVYVDPDETRIKHLRVFETTAWSIFAYIMLYMILAVFSPGVQV 278  
 QY 232 WEGILLTFEPFVVCVLLAMVADKRLFFYMKKRTDKRGIIETEDDKRG---IEMDKMNSH 290  
 DB 279 WEGILLTFEPFVVCVLLAMVADKRLFFYMKKRTDKRGIIETEDDKRG---IEMDKMNSH 334  
 QY 291 ---MNSHFLDGNLPLLEGEKVD---ESRREIRILDKOKHPKEDDOLVEMANYALSH 345  
 DB 335 GPKOPWTS--ARGN---DAEAFDEARREYITLTTELKOKHPKEDDOLVEMANYALSH 388  
 QY 346 HOOKSRAFYRIQATRMATGAGNLIKHAADQAKKASSMEVHDEPE-DFISKVFFDPCSYOC 399  
 DB 389 RSKSRAFYRIQATRMATGAGNLIKHAADQAKKASSMEVHDEPE-DFISKVFFDPCSYOC 445  
 QY 400 FDCPSYOCLENGCAVLLTVVRKGGMSKTMVDTKTEDGSANAGADYETECTVYLAKPE 459  
 DB 446 FDCPSYOCLENGCAVLLTVVRKGGMSKTMVDTKTEDGSANAGADYETECTVYLAKPE 504

[illegible]

QY	665	EESIEFKTTPVKLKKTKTNLALVVGHSNRDGFMEAITVSAGDEDEDESGERLPSCFDY	724
Db	138	EESIEFKTTPDKLKKNLALVVGHSNRDGFMEAITVSAGDEDEDESGERLPSCFDY	197
QY	725	VMHFLTYFMWKLAFACVPPTKCHGACPAVSILITGMLTAIIGDLASHFGCTIGLKDSVT	784
Db	198	VMHFLTYFMWKLAFACVPPTKCHGACPAVSILITGMLTAIIGDLASHFGCTIGLKDSVT	257
QY	785	AVEFVAFGTSPDTFASKAALADVVADASIGNWTGSNAVNVLFIGLAMSVAAIYMALQ	844
Db	258	AVEFVAFGTSPDTFASKAALADVVADASIGNWTGSNAVNVLFIGLAMSVAAIYMALQ	317
QY	845	GQEHVSAGTLAFSVYLFTTFAPVCISVLYRRRPHLGELGGPRGCKLATTMLEFSIML	904
Db	318	GQEHVSAGTLAFSVYLFTTFAPVCISVLYRRRPHLGELGGPRGCKLATTMLEFSIML	377
QY	905	LYILEATLEAVCYIKGF	921
Db	378	LYILEATLEAVCYIKGF	394
RESULT 14			
AAO05893			
ID	AAO05893	standard; Protein: 120 AA.	
XX	AAO05893;		
DT	06-NOV-2001	(first entry)	
DE	Human polypeptide SEQ ID NO 19785.		
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KM	vaccine; peptide therapy; stem cell growth factor; hematopoiesis;		
KM	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KM	nervous system disorders; arthritis; inflammation.		
OS	Homo sapiens.		
XX			

PN W0200164835-A2.  
XX  
PD 07-SEP-2001.  
XX  
PE 26-FEB-2001; 2001WO-US04927.  
XX  
PR 28-FEB-2000; 2000US-0515126.  
XX 18-MAY-2000; 2000US-0577409.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX WPI; 2001-514838/56.  
DR N-PSDB; AA185824.  
XX  
PT Isolated nucleic acids and polypeptides, useful for preventing  
PT diagnosing and treating e.g. leukaemia, inflammation and immune  
PT disorders -  
XX  
PS Claim 20: SEQ ID NO 19785; 1399pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AA179941-AA193841) and  
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhbn activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
XX  
SQ Sequence 120 AA;

Query Match 12.5%; Score 599; DB 22; Length 120;  
Best Local Similarity 100.0%; Pred. No. 4,2e-50;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 757 LIIGMLTAIIGDLASHEGCTIGLDSYAVVFAFGTSVPDPFASKAALQDYYADASIG 816  
DB 1 LIIGMLTAIIGDLASHEGCTIGLDSYAVVFAFGTSVPDPFASKAALQDYYADASIG 60

QY 817 NVTSSNAVNVFLGIGLMSVAIYWAIOGGEFHVSAAGTIAFSVTLFTTFAVCISVLLYR 876  
DB 61 NVTSSNAVNVFLGIGLMSVAIYWAIOGGEFHVSAAGTIAFSVTLFTTFAVCISVLLYR 120

RESULT 15  
AA158044  
ID AA158044 standard; Protein; 539 AA.  
XX  
AC AA158044;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
XX Arabidopsis thaliana 11 transmembrane domain transporter MXH.  
DE  
XX 11 transmembrane domain transporter; MXH; metal cation-proton exchanger;  
KM zinc; magnesium; stress tolerance; transgenic plant.  
XX  
OS Arabidopsis thaliana.  
XX  
PN W09961616-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 25-MAY-1999; 99WO-IL00277.  
XX

PR 26-MAY-1999; 98IL-0124653.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
PA (FLAN-) FLANDER INTERUNIVERSITY INST BIOTECHNOLO.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Gallili G, Shaul O, Inze D, Van Montagu M, Hilgemann DW;  
XX WPI; 2000-062714/05.  
DR N-PSDB; AA247475, AA247476.  
XX  
PT New isolated DNA encoding a metal cation-proton exchanger from plants,  
PT used to produce transgenic plants with improved stress tolerance  
PS Claim 3; Fig 1; 52pp; English.  
XX

CC This is the Arabidopsis thaliana 11 transmembrane domain transporter  
CC designated MXH protein sequence. The MXH protein is a member of the 11-12  
CC transmembrane domain transporter family and has Mg<sup>2+</sup>/H<sup>+</sup> or Zn<sup>2+</sup>/H<sup>+</sup>  
CC exchange activity. In plants Mg<sup>2+</sup> and Zn<sup>2+</sup> are essential for the  
CC integrity of ribosomes and cellular function require a fine balance of  
CC various ions including magnesium and zinc. The polypeptide and nucleotide  
CC sequences of MXH can be used to transform plant cells and produce  
CC transgenic plants. The transformed plants have improved tolerance to  
CC stress conditions such as drought, temperature, mineral excess or  
CC deficiency and high salinity. Other improvements include better growth  
CC on calcareous soils, possibly also improved uptake of important metals  
CC where these have limited availability in the soil.  
XX  
SQ Sequence 539 AA;

Query Match 12.1%; Score 579; DB 21; Length 539;  
Best Local Similarity 22.3%; Pred. No. 5e-47;  
Matches 191; Conservative 110; Mismatches 199; Indels 356; Gaps 22;

QY 64 YPENPSGDKTARIVYFVALITYMFLGVSTIADFFMASIEVYISQREYTIKPKNGTST 123  
DB 29 FPGENTLSDDL-RCGLVFLGLAYCFIGLSAITARFFKSMENVVHSHKRYVTIDPTRAEV 87

QY 124 TTI-RVNNERYSNLTLMAGSSAPEILLILEY---CGHGFIADLPSTIVGSAANMF 179  
DB 88 ITTKVNNFTIADISLAFGSPFOISLATIDAIRNMGERY-AGGLDPGTVLSAARDLF 146

QY 180 IIGICVYVYPDGETRKIKHLRFETFAWSIFAYIMLYMLAVSPGVQVWBGELTLF 239  
DB 147 PIHAVCVVPRAGELKIKSIDGLVGLVWLSFMAYIMLYITLEVSPNVITLVEALLTVL 206

QY 240 FFVYCVLLAVVAOKRLLEFYKYMKKYRTDKHGIITETGDPKIGIMDKMNSHFLDG 299  
DB 207 QYGLLVHAYAOQKR--WPTLS-----LPMRSGDRPE----- 236

QY 300 NLVPLEGKEWDESRREMIRILKDKQKHPKDLQVLWMANYVALSHQKSRARFRIQAT 359  
DB 237 EWPV---EIDITRK-----DDNDND----- 253

QY 360 RMTAGNIIKKHAAEQAKRASSMEVHTDEPEDFISKVEFPDPCSYOCLENGAVLLTVV 419  
DB 254 -----VHDVYSDAADAIV----- 266

QY 420 RKGDMSKTYVDYKTEGDSANAGADYFTETGVVLKPGETQKEFSVGIIDDDIFEEDEH 479  
DB 267 -----ESGSRN-----IVD----- 275

QY 480 FFVLSNVRIEEDPEEGMPPAIFNSLPRLRAVLASPCAVTITLDDDHGIGTFEEDTI 539  
DB 276 -----II-----II----- 279

QY 540 HVSESIGMEVKVLTSGANGTVIVPRVEGTAKGSGEDEDYTGELFKNDETVTIR 559  
DB 280 H-----SANNDCITHTYADPP-----DSATKKGK 306

QY 600 VKIVDEEYERQENFTALGPCKMERGISDYDTRKILMEEEKARIAEKGPVLGEHPK 659

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Db 307 AK----- 308
Qy 660 LEVIESEYFKTVDKLIKTNLALVGHSHRDOFMEATVSAAGDEDESEGERLP 719
Db 309 -----NSTVPDI-----WKHOFVDATVLETSESKVD-SYLRJA 342
Qy 720 SCFDYVMHFLTVFWKVLFAVCVPTPEYCHGWACPAVSLIIGMLTAITGDLASHFGCTIGL 779
Db 343 KSF---WHILLAPWKLLFAFVPPCNIAHGMIAFICSLFISGVAFYVTRFTDLISCVTGI 399
Qy 780 KDSVTAVVFVAGTSVPTFPASKAALQDVYADASTIGNVTSNAVNVFLGIGLAMSVAAT 839
Db 400 NPVIAFTALASGTSWPDVASKIAEROLTADSAIANITCSNSVNIYVIGVPMLINTV 459
Qy 840 --YWALOGGEFHSAGTFLAFSVTLFTIIFAVCISVLLYRRRPHLGELGPGRCCKLATW 897
Db 460 YNFFAIREPLYENAKGLSPSLIFPATSVCIVLVLRRLL-ITGAELGGPRLMAMLTSA 518
Qy 898 LFVSLMLLYILFATLE 913
Db 519 YFMMLMVVFVLSLTK 534

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